Amendment to the Specification:

Please replace the paragraph at page 11 lines 6-17 with the following paragraph:

The Expect value is used as a convenient way to create a significance threshold for reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0, the Expect value is also used instead of the P value (probability) to report the significance of matches. For example, an E value of one assigned to a hit can be interpreted as meaning that in a database of the current size one might expect to see one match with a similar score simply by chance. An E value of zero means that one would not expect to see any matches with a similar score simply by chance. ~~See, BLAST at the National Library of Medicine website.~~ Occasionally, a string of X's or N's will result from a BLAST search. This is a result of automatic filtering of the query for low-complexity sequence that is performed to prevent artifactual hits. The filter substitutes any low-complexity sequence that it finds with the letter "N" in nucleotide sequence (e.g., "NNNNNNNNNNNNN") or the letter "X" in protein sequences (e.g., "XXXXXXXXX"). Low-complexity regions can result in high scores that reflect compositional bias rather than significant position-by-position alignment. Wootton and Federhen, Methods Enzymol 266:554-571, 1996.

Please replace the paragraph at page13 lines 7-16 with the following paragraph:

The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro ~~website~~ <u>database (Mulder N.J., Apweiler R., Attwood T.K., Bairoch A., Barrell D., Bateman A., Binns D., Biswas M., Bradley P., Bork P., Bucher P., Copley R.R., Courcelle E., Das U., Durbin R., Falquet L., Fleischmann W., Griffiths-Jones S., Haft D., Harte N., Hulo N., Kahn D., Kanapin A., Krestyaninova M., Lopez R., Letunic I., Lonsdale D., Silventoinen V., Orchard S.E., Pagni M., Peyruc D., Ponting C.P., Selengut J.D., Servant F., Sigrist C.J.A., Vaughan R, Zdobnov E.M. (2003). *The InterPro Database, 2003 brings increased coverage and new features.* Nucl. Acids. Res. 31: 315-318.)</u> A NOV1 protein contains the following protein domains (as defined by Interpro) at the indicated nucleotide positions: ZU5 domain (IPR000906) at amino acid positions 495 to 598, Thrombospondin type I domain (IPR000884) at amino acid positions 246 to 295, Death domain (IPR000488) at amino acid positions 817 to 897, Immunoglobulin domain (IPR003006) at amino acid positions 163 to 223, Somatotropin hormone family (IPR001400) at amino acid positions 372 to 389, Keratin, high sulfur B2 protein (IPR002494) at amino acid positions 232 to 348.

Please replace the paragraph at page 14, lines 14-18 with the following paragraph:

Somatotropin is a hormone that plays an important role in growth control. It belongs to a family that includes choriomammotropin (lactogen), its placental analogue; prolactin, which promotes lactation in the mammary gland, and placental prolactin-related proteins; proliferin and proliferin related protein; and somatolactin from various fish.[[.]] The 3D structure of bovine somatotropin has been predicted using a combination of heuristics and energy minimization.

Please replace the paragraph at page 78 lines 5 and 12 with the following paragraph:

The relatedness of amino acid families may also be determined based on side chain interactions. Substituted amino acids may be fully conserved "strong" residues or fully conserved "weak" residues. The "strong" group of conserved amino acid residues may be any one of the following groups: STA, NEQK (SEQ ID NO:62) , NHQK (SEQ ID NO:63) , NDEQ (SEQ ID NO:64) , QHRK (SEQ ID NO:65) , MILV(SEQ ID NO:66) , MILF (SEQ ID NO:67), HY, FYW, wherein the single letter amino acid codes are grouped by those amino acids that may be substituted for each other. Likewise, the "weak" group of conserved residues may be any one of the following: CSA, ATV, SAG, STNK (SEQ ID NO:68) , STPA (SEQ ID NO:69) , SGND (SEQ ID NO:70) , SNDEQK (SEQ ID NO:71) , NDEQHK (SEQ ID NO:72), NEQHRK (SEQ ID NO:73) , VLIM (SEQ ID NO:74), HFY, wherein the letters within each group represent the single letter amino acid code.